glycine and benzoylsarcosine is essentially complete, *i. e.*

$$C_6H_5CONR_1CH_2CO_2H + 2H_2SO_4 \rightleftharpoons \left[C_6H_5C(=O)=NR_1CH_2CO\right]^+ + H_3O^+ + 2HSO_4^-$$

(R_1 = H, CH_3; i = 4)

The similarity in the behavior of the latter two solutes is not disconcerting for there is no feature of any one of the reaction steps which would render the N-methyl compound incapable of cyclization. Indeed this situation may not be unique, for we regard as inconclusive the evidence[8,9] upon which is based the repeated claim[7,8,10] that acylsarcosines cannot cyclize in acetic anhydride.

It has been observed that the acid catalyzed cyclization of α-acylamino acids can also be conducted in the solvent acetic anhydride. Further observations on the cyclization of acylsarcosines and some preparative applications of the above observations will be reported in a subsequent communication.

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(9) V. Deulofeu, *Ber.*, **67**, 1542 (1934).
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GATES AND CRELLIN LABORATORIES OF CHEMISTRY
CALIFORNIA INSTITUTE OF TECHNOLOGY
PASADENA, CALIFORNIA JOSEPH L. O'BRIEN
CONTRIBUTION NO. 1466 CARL NIEMANN
RECEIVED AUGUST 28, 1950

TWO HYDROGEN-BONDED SPIRAL CONFIGURATIONS OF THE POLYPEPTIDE CHAIN

Sir:

During the past fifteen years we have been carrying on a program of determination of the detailed atomic arrangements of crystals of amino acids, peptides, and other simple substances related to proteins, in order to obtain structural information that would permit the precise prediction of reasonable configurations of proteins. We have now used this information to construct two hydrogen-bonded spiral configurations of the polypeptide chain, with the residues all equivalent, except for variation in the side chain.

We have attempted to find all configurations for which the residues have the interatomic distances and bond angles found in the simpler substances and are equivalent, and for which also each CO group and NH group is involved in the formation of a hydrogen bond. The plane layer of extended polypeptide chains is a structure of this type, the hydrogen bonds being formed between adjacent chains. In addition there are two spiral structures, in which the plane of the conjugated system C–CO–NH–C is nearly parallel to the spiral axis, and hydrogen bonds are formed between each carbonyl and imino group and an imino or carbonyl group of a residue nearly one turn forward or back along the spiral.

One of these spirals is the three-residue spiral, in which there are about 3.7 residues per turn and each residue is hydrogen-bonded to the third residue from it in each direction along the chain. The unit translation per residue is 1.47 Å. There is evidence that indicates strongly that this configuration is present in α-keratin, contracted myosin, and some other fibrous proteins and also in hemoglobin and other globular proteins.[1]

The second hydrogen-bonded spiral is the five-residue spiral, in which there are about 5.1 residues per turn and each residue is hydrogen-bonded to the fifth residue from it in each direction. The unit translation is 0.96 Å. We believe that this spiral is present in supercontracted keratin, which is formed from α-keratin with a shrinkage of about 35% in the fiber direction.

We are indebted to Drs. H. R. Branson and S. Weinbaum for assistance. Our work has been aided by grants from the Rockefeller Foundation and the National Foundation for Infantile Paralysis. A detailed account of the work will be published soon.

(1) A three-residue spiral described by Huggins (*Chem. Rev.*, **32**, 211 (1943)) is similar to ours, but differs from it in essential structural details.

GATES AND CRELLIN LABORATORIES OF CHEMISTRY
CALIFORNIA INSTITUTE OF TECHNOLOGY
PASADENA 4, CALIFORNIA LINUS PAULING
CONTRIBUTION NO. 1481 ROBERT B. COREY
RECEIVED OCTOBER 16, 1950

CHEMICAL NATURE AND SYNTHESIS OF THE *LACTOBACILLUS BULGARICUS* FACTOR[1]

Sir:

The presence of 65–75% of bound pantothenic acid in concentrates of the *Lactobacillus bulgaricus* factor (LBF)[2] indicated that the unidentified portion(s) of the molecule must be relatively small in size. Hydrolysates of such preparations[2] had an unpleasant odor reminiscent of sulfur compounds. Application of the iodine-azide reagent[3] to paper chromatograms of LBF confirmed the presence of sulfur. In acid hydrolysates, a sulfur-containing fragment that also gave a color with ninhydrin and with nitroprusside–cyanide reagent appeared on papergrams. Since LBF is essentially neutral and is not destroyed by nitrous acid[4] it contains no free amino or carboxyl groups. An amide linkage between pantothenic acid and a mercaptoamine (or the corresponding disulfide) is thus indicated. Biogenetic and analytical considerations pointed to β-mercaptoethylamine as a possible fragment. Pure β-mercaptoethylamine[5] showed the same R_F value on papergrams (0.43;

(1) Supported in part by grants from Parke, Davis and Co., and the National Institutes of Health.
(2) G. M. Brown, J. A. Craig and E. E. Snell, *Arch. Biochem.*, **27**, 473 (1950).
(3) E. Chargaff, C. Levine and C. Green, *J. Biol. Chem.*, **175**, 67 (1948).
(4) W. L. Williams, E. Hoff-Jorgensen and E. E. Snell, *ibid.*, **177**, 933 (1949).
(5) E. J. Mills and M. T. Bogert, THIS JOURNAL, **62**, 1173 (1940).